

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 21:34:03 ; Search time 44 Seconds
(without alignments)
2359.216 Million cell updates/sec

Title: US-10-081-775-2

Perfect score: 1718

Sequence: 1 MSSTLGHNMESPHHTDVPF.....RKVRVRFQSGQGMKASE 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_protist:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1534	89.3	329	11 Q8VGV9	Q8VGV9 mus musculus
2	1517	88.3	321	11 Q7TRP8	Q7TRP8 mus musculus
3	977.5	56.9	315	11 Q8VGV23	Q8VGV23 mus musculus
4	936.5	54.5	299	4 Q8NGF2	Q8NGF2 homo sapien
5	936	54.5	316	11 Q7TRN7	Q7TRN7 mus musculus
6	927	54.0	317	11 Q8VGV8	Q8VGV8 mus musculus
7	912.5	53.1	319	11 Q7TRS6	Q7TRS6 mus musculus
8	907.5	52.8	317	11 Q8VEX9	Q8VEX9 mus musculus
9	891.5	51.9	311	11 Q7TRR4	Q7TRR4 mus musculus
10	890.5	51.8	317	11 Q8VGV5	Q8VGV5 mus musculus
11	890.5	51.8	323	11 Q8VGV5	Q8VGV5 mus musculus
12	890	51.8	314	11 Q8VGV22	Q8VGV22 mus musculus
13	890	51.8	318	11 Q8VGV1	Q8VGV1 mus musculus
14	887.5	51.7	316	11 Q8VGV79	Q8VGV79 mus musculus
15	887.5	51.7	318	11 Q8VGV3	Q8VGV3 mus musculus
16	887.5	51.7	326	11 Q9WVD9	Q9WVD9 mus musculus

17	883.5	51.4	317	11 Q8VGV9	Q8VGV9 mus musculus
18	883	51.4	316	11 Q7TRRS	Q7TRRS mus musculus
19	883	51.4	327	11 Q8VF28	Q8VF28 mus musculus
20	883	51.4	339	11 Q9WU90	Q9WU90 mus musculus
21	882.5	51.4	312	11 Q8VGV2	Q8VGV2 mus musculus
22	881.5	51.3	317	11 Q8VH04	Q8VH04 mus musculus
23	880.5	51.3	312	11 Q7TRR6	Q7TRR6 mus musculus
24	877.5	51.1	316	11 Q7TRQ8	Q7TRQ8 mus musculus
25	877	51.0	341	11 Q8VF27	Q8VF27 mus musculus
26	875	50.9	314	11 Q7TRR0	Q7TRR0 mus musculus
27	873.5	50.8	312	11 Q8VGV4	Q8VGV4 mus musculus
28	873	50.8	317	11 Q8VGV7	Q8VGV7 mus musculus
29	871.5	50.7	316	11 Q8VGV24	Q8VGV24 mus musculus
30	871	50.7	319	11 Q8VGV9	Q8VGV9 mus musculus
31	871	50.7	324	11 Q7TRP9	Q7TRP9 mus musculus
32	870	50.6	314	11 Q7TRRS2	Q7TRRS2 mus musculus
33	868.5	50.6	312	11 Q8VFO6	Q8VFO6 mus musculus
34	868.5	50.6	319	11 Q8VGV0	Q8VGV0 mus musculus
35	867.5	50.5	314	11 Q7TRS0	Q7TRS0 mus musculus
36	866	50.4	314	11 Q8EQQ6	Q8EQQ6 mus musculus
37	865	50.3	316	11 Q8VH03	Q8VH03 mus musculus
38	865	50.3	320	11 Q8VBV9	Q8VBV9 mus musculus
39	864.5	50.3	312	11 Q7TRP3	Q7TRP3 mus musculus
40	860.5	50.1	308	11 Q8VGV84	Q8VGV84 mus musculus
41	858	49.9	314	11 Q7TRR7	Q7TRR7 mus musculus
42	854	49.7	314	11 Q8VEW8	Q8VEW8 mus musculus
43	852	49.6	318	11 Q8VH00	Q8VH00 mus musculus
44	851.5	49.6	317	4 Q8NGK5	Q8NGK5 homo sapien
45	851	49.5	322	11 Q8VGV5	Q8VGV5 mus musculus

ALIGNMENTS

RESULT 1

Q8VGV9	PRELIMINARY;	PRT;	329 AA.
ID Q8VGV9			
AC Q8VGV9			
DT 01-MAR-2002 (Tremblrel. 20, Created)			
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)			
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)			
DE Olfactory receptor MOR27-1.			
OS Mus musculus (Mouse)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Zhang X., Firestein S.J.;			
RT "The olfactory receptor gene superfamily of the mouse."			
RL Nat. Neurosci. 0:0-0(2002).			
RN [2]			
RP SEQUENCE FROM N.A.			
RA Adams M.;			
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR EMBL, AY073012; AAL60675.1; -			
DR GO; GO:0046021; C:integral to membrane; IEA.			
DR GO; GO:0004872; F:receptor activity; IEA.			
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.			
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.			
DR InterPro; IPR000276; GPCR_Rhodopsn.			
DR Pfam; PF00001; 7tm_1; 1.			
DR PRINTS; PR00237; GPCR_Rhodopsn.			
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; 1.			
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2_1; 1.			
DR KW Receptor.			
SQ SEQUENCE 329 AA; 36285 MW; 7D23203F650861EF CRC64;			

Query Match 89.3%; Score 1534; DB 11; Length 329;

Best Local Similarity 88.1%; Pred. No. 8.8e-135;

Matches 290; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

QY 1 MSSTLGHNMESPHHTDVPF.....RKVRVRFQSGQGMKASE 60

Db 1 MSNTISQTESPHNDLPSIFLLGIGLGFQFHMWLSLPVCCUGTATVGNITILVVVA 60
 QY 61 TEPLHKEPVYLFLOMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFIHAFCMM 120
 Db 61 TEPLHKEPVYLFLOMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFIHAFCMM 120
 QY 121 ESTVLLAMAPDYVAICHLPLRYATILDTTIIAHGVAAVRGSLMLPCPFIFGLNFCQ 180
 Db 121 ESTVLLAMAPDYVAICHLPLRYATILDTTIIAHGVAAVRGSLMLPCPFIFGLNFCQ 180
 QY 181 SHVLHTYCEHMAVVKLACGDTNRNVYGLTAALLVIGVDLFCIGLSYALLAQAVRLSS 240
 Db 181 SHVLHTYCEHMAVVKLACGDTNRNVYGLTAALLVIGVDLFCIGLSYALLAQAVRLSS 240
 QY 241 HEARSKALGTCGSHVCVILISYTPALFSFFTHRGHVPVHIIHANVYLLPPALNPV 300
 Db 241 HEARSKALGTCGSHVCVILISYTPALFSFFTHRGHVPVHIIHANVYLLPPALNPV 300
 QY 301 VYGKTKOIRKVRVVFQSGQMGKIKASE 329
 Db 301 VYGKTKOIRKVRVVFQSGQMGKIKASE 329

RESULT 2

Q7TRP8 PRELIMINARY; PRT; 321 AA.
 ID AC Q7TRP8
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DE Olfactory receptor GA_x6K02T2PB9-7245486-7245451.
 GN GA_X6K02T2PB9-7245486-7245451.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
 Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY317777; AAF71129.1; --
 KW Receptor.
 SQ SEQUENCE 321 AA; 35422 MW; 7E5B78779DEC4D0F CRC64;

Query Match 88.3%; Score 1517; DB 11; Length 321;
 Best Local Similarity 89.4%; Pred. No. 3.3e-133;
 Matches 287; Conservative 16; Mismatches 18; Indels 0; Gaps 0;
 QY 9 MESPHHTDVPDSVFFLLGIPGLEQFHLWLSLPVCGLTATVGNITILVVVATEPVLHXP 68
 Db 1 MESPHHTDVPDSVFFLLGIPGLEQFHLWLSLPVCGLTATVGNITILVVVATEPVLHXP 68
 QY 69 VYLFCLMSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFIHAFCMMESTVLLAM 128
 Db 61 VYLFCLMSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFIHAFCMMESTVLLAM 128
 QY 129 AFDRYVAICHLPLRYATILDTTIIAHGVAAVRGSLMLPCPFIFGLNFCQSHVILHTY 188
 Db 121 AFDRYVAICHLPLRYATILDTTIIAHGVAAVRGSLMLPCPFIFGLNFCQSHVILHTY 188
 QY 189 CEHMAVVKLACGDTNRNVYGLTAALLVIGVDLFCIGLSYALLAQAVRLSSSQRASKAL 248
 Db 191 CEHMAVVKLACGDTNRNVYGLTAALLVIGVDLFCIGLSYALLAQAVRLSSSQRASKAL 248
 QY 248 GTCGSHVCVILISYTPALFSFFTHRGHVPVHIIHANVYLLPPALNPV 300

Db 241 GTCGSHVCVILISYTPALFSFFTHRGHVPVHIIHANVYLLPPALNPV 300
 QY 309 IRREVVRVVFQSGQMGKIKASE 329
 Db 301 IRREVVRVVFQSGQMGKIKASE 329

RESULT 3

Q8VG23 PRELIMINARY; PRT; 315 AA.
 ID AC Q8VG23
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DE Olfactory receptor MOR29-1 (Olfactory receptor
 GA_X6K02T2PB9-5307445-5306498).
 GN GA_X6K02T2PB9-5307445-5306498.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
 Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY317664; AAF71043.1; --
 DR EMBL; AY317664; AAF71043.1; --
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signaling; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 315 AA; 34242 MW; 0926C74DB9A4470C CRC64;

Query Match 56.9%; Score 977.5; DB 11; Length 315;
 Best Local Similarity 56.4%; Pred. No. 6.1e-83;
 Matches 176; Conservative 56; Mismatches 79; Indels 1; Gaps 1;
 QY 9 MESPHHTDVPDSVFFLLGIPGLEQFHLWLSLPVCGLTATVGNITILVVVATEPVLHXP 68
 Db 1 MESPHHTDVPDSVFFLLGIPGLEQFHLWLSLPVCGLTATVGNITILVVVATEPVLHXP 68
 QY 69 VYLFCLMSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFIHAFCMMESTVLLAM 128
 Db 61 VYLFCLMSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFIHAFCMMESTVLLAM 128
 QY 129 AFDRYVAICHLPLRYATILDTTIIAHGVAAVRGSLMLPCPFIFGLNFCQSHVILHTY 188
 Db 121 AFDRYVAICHLPLRYATILDTTIIAHGVAAVRGSLMLPCPFIFGLNFCQSHVILHTY 188